

REMARKS

1. Status of the Claims and Formal Matters

Claims 1-16 are pending in this application. Claims 11-12 and 15 are withdrawn from further consideration. Claims 3 and 6 are hereby cancelled without prejudice to pursuing these claims in a continuing application. Claims 1-2, 4-5, 7-10 and 14 are amended. Upon entry of these amendments, claims 1-2, 4-5 and 7-16 are pending with claims 1-2, 4-5, 7-10, 13-14 and 16 under active consideration. Applicants respectfully request entry of the amendments and remarks made herein into the file history of the present application.

The specification is amended at page 1 to add a reference to each earlier filed application for which the benefit of an earlier filing date is claimed.

The specification is amended at paragraph [0050] to add sequence identifiers to the disclosed sequences.

The specification is amended at paragraph [0053] to add sequence identifiers to the disclosed sequences.

The specification is amended at paragraph [0056] to add sequence identifiers to the disclosed sequences.

The specification is amended at paragraph [0193] to add sequence identifiers to the disclosed sequences.

The specification is amended at paragraph [0198] to correct typographical errors and add sequence identifiers to the disclosed sequences.

The specification is amended at paragraph [0200] to correct typographical errors and add sequence identifiers to the disclosed sequences.

The specification is amended at paragraph [0203] to add sequence identifiers to the disclosed sequences.

The specification is amended at paragraph [0206] to add sequence identifiers to the disclosed sequences.

Claim 1 is amended to recite an "isolated" gene, support for which may be found at paragraphs [0008] and [0009]. Claim 1 is also amended to recite that the gene is a human gene, support for which may be found throughout the specification. Claim 1 is also amended to recite that the gene encodes an RNA of about 50 to about 120 nucleotides, support for which may be

found at claim 1 as originally filed. Claim 1 is also amended to recite that 18 to 24 nucleotides of a first portion of the encoded RNA are at least 50% complimentary to 18 to 24 nucleotides of a second portion of the encoded RNA, support for which may be found at Table 1 and paragraph [0011]. Claim 1 is also amended to recite that at least one of the first or second portion of the RNA is at least 60% complimentary to 18 to 24 nucleotides of a target human gene, support for which may be found at Table 2 and paragraph [0011].

Claim 2 is amended to recite an isolated gene that comprises a plurality of genes according to claim 1, support for which may be found throughout the specification, notably at Figure 6 and claim 2 as originally filed.

Claim 4 is amended to recite the gene of claim 1 is maternally transferred by a cell to at least one daughter cell of said cell, support for which may be found at claim 4 as originally filed.

Claim 5 is amended to recite that expression of the gene of claim 1 is capable of promoting expression of the target gene, support for which may be found at claim 5 as originally filed.

Claim 7 is amended to recite that the RNA encoded by the DNA of claim 1 is capable of modulating expression of the target gene, support for which may be found at claim 7 as originally filed.

Claim 8 is amended to recite that the binding site sequence of the target human gene is located in an untranslated region of the RNA encoded by the target gene, support for which may be found at claim 8 as originally filed.

Claim 9 is amended to recite that the binding site sequence of the target gene is located in the 3' untranslated region of the RNA encoded by the target gene, support for which may be found at paragraph [0097].

Claim 10 is amended to correct antecedent basis.

Claim 13 is amended to recite that the gene expression inhibition system comprises a vector of claim 10, support for which may be found at claim 13 as originally filed. Claim 13 is also amended to recite that the gene expression inhibition system comprises a means for inserting the vector into a cell, support for which may be found at paragraph [0023] and claim 13 as originally filed.

Claim 14 is amended to correct antecedent basis.

2. Patentability Objections – Sequence Rules

At page 2 of the Office Action, the Examiner objects to the disclosure for allegedly failing to comply with the requirements set forth in 37 C.F.R. §§ 1.821-1.825 (the “Sequence Rules”). The specification has been amended to provide sequence identifiers for recited sequences, as set forth above. Accordingly, Applicants respectfully request that the objection for failing to comply with the Sequence Rules be withdrawn.

3. Election

At pages 2-3 of the Office Action, the Examiner requires restriction to one of the following inventions under 35 U.S.C. 121:

- I. Claims 1-10, 13-14 and 16, drawn to a bioinformatically detectable novel gene, a probe comprising said novel gene, a vector comprising said novel gene, a kit comprising said vector and a vector inserter and a kit comprising said probe and a gene expression detector.
- II. Claims 11 and 12, drawn to a method of inhibiting translation of at least one gene comprising introducing the vector of claim 10 into a cell.
- III. Claim 15, drawn to a method of detecting gene expression using a DNA probe that comprises a bioinformatically detectable novel gene.

Applicants elect without traverse Group I, claims 1-10, 13-14 and 16, drawn to a bioinformatically detectable novel gene, a probe comprising said novel gene, a vector comprising said novel gene, a kit comprising said vector and a vector inserter and a kit comprising said probe and a gene expression detector.

4. Conclusion

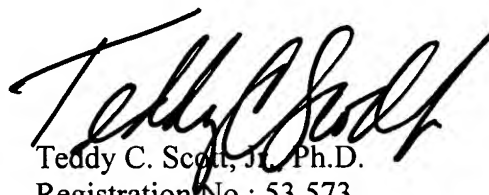
Applicant respectfully submits that the instant application is in good and proper order for allowance and early notification to this effect is solicited. If, in the opinion of the Examiner, a telephone conference would expedite prosecution of the instant application, the Examiner is encouraged to call the undersigned at the number listed below.

Respectfully submitted,

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APPENDIX A

For the convenience of the Examiner, Applicant presents herewith a copy of the claims that will be pending upon entry of the present amendments.

1. (currently amended) An isolated A bioinformatically detectable novel human gene encoding ~~substantially pure DNA wherein: RNA encoded by said bioinformatically detectable novel gene is about 18 to about 24 nucleotides in length, and originates from an RNA precursor, which RNA precursor is of about 50 to about 120 nucleotides, in length; a nucleotide sequence of wherein a first portion of the RNA of 18 to 24 nucleotides is at least 50% complementary to a second portion of the RNA sequence of 18 to 24 nucleotides, a first half of said RNA precursor is a partial inversed reversed sequence of a nucleotide sequence of a second half thereof; and wherein at least one of the first or second portion of the RNA is at least 50% complementary to a binding site sequence of 18 to 24 nucleotides of a target human gene a nucleotide sequence of said RNA encoded by said novel gene is a partial inversed reversed sequence of a nucleotide sequence of a binding site associated with at least one target gene; said novel gene cannot be detected by either of the following: a visually discernable whole body phenotype; and detection of 99.9% of RNA species shorter than 25 nucleotides expressed in a tissue sample; and a function of said novel gene is bioinformatically deducible.~~

2. (currently amended) An isolated A bioinformatically detectable novel human gene comprising encoding substantially pure DNA wherein: RNA encoded by said bioinformatically detectable novel gene comprises a plurality of genes according to claim 1 ~~RNA sections, each of said RNA sections being about 50 to about 120 nucleotides in length, and comprising an RNA segment, which RNA segment is about 18 to about 24 nucleotides in length; a nucleotide sequence of a first half of each of said RNA sections encoded by said novel gene is a partial inversed reversed sequence of nucleotide sequence of a second half thereof; a nucleotide sequence of each of said RNA segments encoded by said novel gene is a partial inversed reversed sequence of the nucleotide sequence of a binding site associated with at least one target gene; and a function of said novel gene is bioinformatically deducible from the following data elements: said nucleotide sequence of said RNA encoded~~

~~by said novel gene, a nucleotide sequence of said at least one target gene, and function of said at least one target gene.~~

3. (canceled)

4. (currently amended) The gene of claim 1, wherein said A bioinformatically detectable novel gene encoding substantially pure DNA wherein: said bioinformatically detectable novel gene does not encode a protein; RNA encoded by said bioinformatically detectable novel gene is maternally transferred by a cell to at least one daughter cell of said cell; a function of said novel gene comprises modulation of a cell type of said daughter cell; and said modulation is bioinformatically deducible.

5. (currently amended) The gene of claim 1, wherein expression of said A bioinformatically detectable novel gene encoding substantially pure DNA wherein: said bioinformatically detectable novel gene does not encode a protein; a function of said novel gene is capable of promoting promotion of expression of said at least one target gene; and said at least one target gene is bioinformatically deducible.

6. (canceled)

7. (currently amended) ~~A bioinformatically detectable novel~~ The gene according to claim 1 and wherein said encoded RNA encoded by said novel gene complementarily binds said binding site associated with said at least one target gene, thereby is capable of modulating expression of said at least one target gene.

8. (currently amended) ~~A bioinformatically detectable novel~~ The gene according to claim 1 and wherein[[:]] said binding site sequence associated with at least one target gene is located in an untranslated region of RNA encoded by said at least one target gene.

9. (currently amended) ~~A bioinformatically detectable novel gene according to claim 7 and wherein: said function of said novel gene is selective inhibition of translation of said at least one target gene, which selective inhibition comprises complementary hybridization of said RNA encoded by said novel gene to said binding site~~ The gene according to claim 8 wherein the binding site sequence is located in the 3'untranslated region of the RNA encoded by said target human gene..

10. (currently amended) A vector comprising the ~~DNA~~ gene of claim 1.

11. (withdrawn) A method of selectively inhibiting translation of at least one gene, comprising introducing the vector of claim 10 into a cell.

12. (withdrawn) A method according to claim 11 and wherein said introducing comprises utilizing RNAi pathway.

13. (currently amended) A gene expression inhibition system comprising[[:]] the vector of claim 10[[:]] and a means for inserting ~~vector inserter, functional to insert~~ said vector ~~of claim 10~~ into a cell, ~~thereby selectively inhibiting translation of at least one gene.~~

14. (currently amended) A probe comprising the ~~DNA~~ gene of claim 1.

15. (withdrawn) A method of selectively detecting expression of at least one gene, comprising using the probe of claim 14.

16. (original) A gene expression detection system comprising: the probe of claim 14; and a gene expression detector functional to selectively detect expression of at least one gene.